

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 08/252,384B
Source: IFW16
Date Processed by STIC: 3-18-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/18/2005

PATENT APPLICATION: US/08/252,384B

TIME: 10:13:00

Input Set : A:\05.0225 RACT00100 08,252,384 Sequence Listing.txt

Output Set: N:\CRF4\03182005\H252384B.raw

3 <110> APPLICANT: Reactive Surfaces, Ltd.

5 <120> TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods of

Use

7 <130> FILE REFERENCE: RACT-00100

C--> 9 <140> CURRENT APPLICATION NUMBER: US/08/252,384B

C--> 10 <141> CURRENT FILING DATE: 1994-06-01

12 <150> PRIOR APPLICATION NUMBER: 07/928,540

13 <151> PRIOR FILING DATE: 1992-08-13

15 <150> PRIOR APPLICATION NUMBER: 08/252,384

16 <151> PRIOR FILING DATE: 1994-06-01

18 <150> PRIOR APPLICATION NUMBER: 07/344,258

19 <151> PRIOR FILING DATE: 1989-04-27

21 <160> NUMBER OF SEQ ID NOS: 2

23 <170> SOFTWARE: PatentIn version 3.3

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 1014

27 <212> TYPE: DNA

28 <213> ORGANISM: Pseudomonas diminuta

31 <220> FEATURE:

32 <221> NAME/KEY: CDS

33 <222> LOCATION: (1)..(1011)

35 <400> SEQUENCE: 1

36 atg tcg atc ggc aca ggc gat cgg atc aat acc gtg cgc ggt cct atc 48

37 Met Ser Ile Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile

38 1 5 10 15

40 aca atc tct gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc 96

41 Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly

42 20 25 30

44 agc tcg gca gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc 144

45 Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg

46 35 40 45

48 aaa gct cta gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg 192

49 Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala

50 50 55 60

52 gct ggc gtg cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc 240

53 Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg

54 65 70 75 80

56 gac gtc agt tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc 288

57 Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile

58 85 90 95

60 gtg gcg gcg acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg 336

61 Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu

62 100 105 110

64 agg agt gta gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat 384

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65 Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
66      115      120      125
68 ggc atc gaa gac acc gga att agg gcg ggc att atc aag gtc gcg acc      432
69 Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
70      130      135      140
72 aca ggc aag gcg acc ccc ttt cag gag tta gtg tta aag gcg gcc gcc      480
73 Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
74 145      150      155      160
76 cgg gcc agc ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca      528
77 Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
78      165      170      175
80 agt cag cgc gat ggt gag cag cag gcc gcc att ttt gag tcc gaa ggc      576
81 Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
82      180      185      190
84 ttg agc ccc tca cgg gtt tgt att ggt cac agc gat gat act gac gat      624
85 Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
86      195      200      205
88 ttg agc tat ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta      672
89 Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
90      210      215      220
92 gac cac atc ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca      720
93 Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
94 225      230      235      240
96 tca gcc ctc ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc      768
97 Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
98      245      250      255
100 aag gcg ctc atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat      816
101 Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
102      260      265      270
104 gac tgg ctg ttc ggg ttt tcg agc tat gtc acc aac atc atg gac gtg      864
105 Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
106      275      280      285
108 atg gat cgc gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg      912
109 Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
110      290      295      300
112 atc cca ttc gta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc      960
113 Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
114 305      310      315      320
116 atc act gtg act aac ccg gcg cgg ttc tat gtc acc gac ctt gcg ggc      1008
117 Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
118      325      330      335
120 gtc atg      1014
121 Val
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 337
127 <212> TYPE: PRT
128 <213> ORGANISM: Pseudomonas diminuta
130 <400> SEQUENCE: 2
132 Met Ser Ile Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile

```

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133 1          5          10          15
136 Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly
137          20          25          30
140 Ser Ser Ala Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg
141          35          40          45
144 Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala
145          50          55          60
148 Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg
149 65          70          75          80
152 Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile
153          85          90          95
156 Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu
157          100         105         110
160 Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr
161          115         120         125
164 Gly Ile Glu Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr
165          130         135         140
168 Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala
169 145          150         155         160
172 Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala
173          165         170         175
176 Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly
177          180         185         190
180 Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp
181          195         200         205
184 Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu
185          210         215         220
188 Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala
189 225          230         235         240
192 Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile
193          245         250         255
196 Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn
197          260         265         270
200 Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val
201          275         280         285
204 Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val
205          290         295         300
208 Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly
209 305          310         315         320
212 Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly
213          325         330         335
216 Val

```

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date